SEQUENCE LISTING

<110> Lin, Xinli

<120> METHODS FOR PRODUCTION OF RECOMBINANT
      UROKINASE

<130> 544112000200

<140> US 10/825,911
<141> 2004-04-16

<150> US 60/463,632
<151> 2003-04-16

<150> US 60/498,134
<151> 2003-08-26

<150> CN 03134847.5
<151> 2003-09-25

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1248
<212> DNA
<213> Homo Sapiens

<400> 1
catatgtcca acgaactgca ccaggttcca tcgaactgtg actgtctaaa tggaggaaca 60
tgtgtgtcca acaagtactt ctccaacatt cactggtgca actgcccaaa gaaattcgga 120
gggcagcact gtgaaataga taagtcaaaa acctgctatg aggggaatgg tcactttttac 180
cgaggaaagg ccagcactga caccatgggc cggccctgcc tgccctggaa ctctgccact 240
gtccttcagc aaacgtacca tgcccacaga tctgatgctc ttcagctggg cctggggaaa 300
cataattact gcaggaaccc agacaaccgg aggcgaccct ggtgctatgt gcaggtgggc 360
ctaaagctgc ttgtccaaga gtgcatggtg catgactgcg cagatggaaa aaagccctcc 420
tctcctccag aagaattaaa atttcagtgt ggccaaaaga ctctgaggcc ccgctttaag 480
attattgggg gagaattcac caccatcgag aaccagccct ggtttgcggc catctacagg 540
aggcaccggg ggggctctgt cacctacgtg tgtggaggca gcctcatcag cccttgctgg 600
gtgatcagcg ccacacactg cttcattgat tacccaaaga aggaggacta catcgtctac 660
ctgggtcgct caaggcttaa ctccaacacg caaggggaga tgaagtttga ggtggaaaac 720
ctcatcctac acaaggacta cagcgctgac acgcttgctc accacaacga cattgccttg 780
ctgaagatcc gttccaagga gggcaggtgt gcgcagccat cccggactat acagaccatc 840
tgcctgccct cgatgtataa cgatccccag tttggcacaa gctgtgagat cactggcttt 900
ggaaaagaga attctaccga ctatctctat ccggagcagc tgaaaatgac tgttgtgaag 960
ctgatttccc accgggagtg tcagcagccc cactactacg gctctgaagt caccaccaaa 1020
atgctgtgtg ctgctgaccc acagtggaaa acagattcct gccagggaga ctcaggggga 1080
cccctcgtct gttccctcca aggccgcatg actttgactg gaattgtgag ctggggccgt 1140
ggatgtgccc tgaaggacaa gccaggcgtc tacacgagag tctcacactt cttaccctgg 1200
atccgcagtc acaccaagga agagaatggc ctggccctct aactcgag 1248

<210> 2
<211> 412
<212> PRT

1

<213> Homo Sapiens

<400> 2

```
Met Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn
 1               5                  10                  15
Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys
             20                  25                  30
Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser
             35                  40                  45
Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser
         50                  55                  60
Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val
65                  70                  75                  80
Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly
                 85                  90                  95
Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro
             100                 105                 110
Trp Cys Tyr Val Gln Val Gly Leu Lys Leu Leu Val Gln Glu Cys Met
         115                 120                 125
Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu
     130                 135                 140
Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile
145                 150                 155                 160
Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala
                 165                 170                 175
Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly
             180                 185                 190
Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile
         195                 200                 205
Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg
     210                 215                 220
Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu
225                 230                 235                 240
Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp
                 245                 250                 255
Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro
             260                 265                 270
Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro
         275                 280                 285
Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser
     290                 295                 300
Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu
305                 310                 315                 320
Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val
                 325                 330                 335
Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser
             340                 345                 350
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg
         355                 360                 365
Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys
     370                 375                 380
Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile
385                 390                 395                 400
Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                 405                 410
```

2

```
<210> 3
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 3
catatgtcca acgaactgca ccaggttcca tcgaactgtg actgtc                46

<210> 4
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4
ctcgagttag agggccaggc cattctcttc                                  30

<210> 5
<211> 1239
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 5
atgagcaatg aactgcatca ggttccgagc aactgtgatt gtctgaatgg tggcacctgt 60
gtgagcaaca atacttcag caacattcac tggtgcaact gcccgaaaaa attcggtggc 120
cagcactgtg aaatcgataa aagcaaaacc tgctatgaag gcaatggtca cttttaccgc 180
ggcaaagcca gcaccgatac catgggccgt ccgtgcctgc cgtggaacag cgccaccgtt 240
ctgcagcaga cctaccatgc ccaccgtagc gatgcgctgc agctgggcct gggtaaacat 300
aattactgcc gcaacccgga taaccgtcgt cgtccgtggt gctatgtgca ggtgggcctg 360
aaaccgctgg ttcaggaatg catggtgcat gattgcgcgg atggtaaaaa accgagcagc 420
ccgccggaag aactgaaatt ccagtgtggc cagaaaaccc tgcgtccgcg ctttaaaatt 480
attggcggcg aattcaccac catcgaaaac cagccgtggt ttgcggccat ctaccgtcgt 540
caccgtggtg gcagcgttac ctacgtgtgt ggtggcagcc tgatcagccc gtgctgggtg 600
atcagcgcca cccactgctt cattgattac ccgaaaaaag aagattacat cgtttacctg 660
ggtcgcagcc gtctgaacag caacacccag ggcgaaatga aatttgaagt ggaaaacctg 720
atcctgcaca aagattacag cgcggatacc ctggcgcacc acaacgatat tgccctgctg 780
aaaatccgta gcaaagaagg ccgttgtgcg cagccgagcc gcaccatcca gaccatctgc 840
ctgccgagca tgtataacga tccgcagttt ggcaccagct gtgaaatcac cggctttggc 900
aaagaaaata gcaccgatta tctgtatccg gaacagctga aaatgaccgt tgtgaaactg 960
attagccacc gtgaatgtca gcagccgcac tactacggca gcgaagtgac caccaaaatg 1020
ctgtgtgcgg cggatccgca gtggaaaacc gatagctgcc agggtgatag cggtggtccg 1080
ctggtttgta gcctgcagtg ccgcatgacc ctgaccggta ttgtgagctg gggccgtggt 1140
tgtgccctga agataaaacc gggcgtttac acccgtgtta gccacttcct gccgtggatc 1200
cgcagccaca ccaaagaaga aaatggcctg gcactgtaa                        1239

<210> 6
<211> 33
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Synthetic Construct

<400> 6
atcactggct ttggacacga gaattctacc gac                                    33


<210> 7
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 7
gtcggtagaa ttctcgtgtc caaagccagt gat                                    33
```